

A

E. coli NuoE MHENQQPQTEAFELSAEREAIEHEMHHYED-
R. prowazekii NuoE MNTKITN--FTFADKKNLNLAEIITIKKYPPE
N. crassa 24 kDa MATKLTFFLMRTAVRAATRLSTKPSIAPVSRACLSISARRPSDTLMVHRNTPDNNPDIFFKFSADNEKVEIEIIKRYPPQ
H. sapiens 24 kDa MFFSAALRARAAGLTAHWGRHVRNLHKTVMQNGAG---GALFVHRDTPENNPDPFDFTPENYKRIEAIVKNYPEG
N. ovalis BA 24 kDa MLSSFILKRTIRPSSFVRMTGYRFSRLVTHHETPENNDTTFEFTPENYKIIINSLKRYPDN
N. ovalis PA HDG YNADESAGLDSILAKYPD-
N. ovalis BD HDG YNVDEAAGLDSILARYPK-
N. ovalis PB HDG YNVDEAAGLDSILARYPK-
N. ovalis BA HDG YNPNEAAGLDEILAKYPK-
N. ovalis PD HDG YNSNEAAGLDEILAKYPK-
N. ovalis PN HDG YNANEAGLDEILAKYPK-
R. opacus HoxF MSGDIKAILERNGS-
R. eutropha HoxF MDSRITITLERYRS-

[2Fe-2S]cluster N1a of

C-----C-----
E.c. NuoE -PRAASIEALKIVQKQRC-WVPDGAIAHADVLGIPASDVEGVATFYSQLFRQPVGRHVRVYCD-SVVVCHIN--GYQCIQAALKKLN
R.p. NuoE GKRSAILPLLDLAQRQNGGWLHVSAIEYVANLEMPYMRAYEVATFYTMFNLPYKGIHQVCT-TTFCWLR--GSDNIMKICEKLLA
N.c. 24 kDa YKKAAMFPLLDLQQRQHG-FCSI SVMNEVARLLEMPMRVYEVASFYTMYNRTPVGFHVAQCT-TTFCQGGCGSDVIVKAIKEHLG
H.s. 24 kDa HKAAAVLPLVLDLAQRQNG-WLPI SAMNKVAELVQVPPMRVYEVATFYTMNRKPVGKYHIQVCT-TTFCMLR--NSDSILEAIIQKLLG
N.o. 24 kDa YKSAVLLYLLHLAQKQNGNFLTAAAMNKVAELVQVPPMRVYEVATFYTMFNLPYKGIHQVCT-TTFCQGGCGSDVIVKAIKEHLG
N.o. PA HDG -HPQYLLPIVIEETDQKG-YISDPSLVKIAKHVHPYPPQVESILSHYHFFPRKYS DTHVYLGR-CHNCMMK--GQSKVMQALKERYG
N.o. BD HDG -HPQYLLPIVIEESDKKG-YISDPSLVKIANHVQMHAPHVESVISHYHFFPRKYS DTHVYLGR-CHNCMMK--GQSKVMQAIKEKYG
N.o. PB HDG -HPQYLLPIVIEESDKKG-YISDPSLVKIANHVQMYAPQVESVISHYHFFPRKYS DTHVYLGR-CHNCMMK--GQSKVMQAIKEKYG
N.o. BA HDG -EREYLLPIVIEEHDKKG-YISDPSIVKISEYLGMPAQIDSILSSYHFFPREHTSDAHVYMC T-CHNCMMK--GQGRLLKTIQETD
N.o. PD HDG -EQEYLLPIVIEEHDKKG-YISDPSIVKISEHLGMPAQIDSILSSYHFFPREHTSDAHVYMC T-CHNCMMK--GQGRLLKTIQETD
N.o. PN HDG -EKEYLMPVIEIEEHDKKG-YISDPSIVKISEHLGMPAQIESILSSYHFFPREHTIATLMSIQVHCHNCMMK--GQGRLLKTIQETD
R.o. HoxF -ERTRLDIDLWDVQHLYG-HIPDEVLPQLADELNLPLDILETASFYHFFRKPSPGKYRIYLS D-TVI AKMN--GYQAVDREALERETG
R.e. HoxF -DRTRLDIDLWDVQHEYG-HIPDAVLPQLGAGLKLSPLDIRETASFYHFFLDKPSGKYRIYLS D-SVI AKIN--GYQAVREALERETG

24 kDa and NuoE

-----C-----
E.c. NuoE IK--PGQTFDGRFTLLPTCCLGNQDK-GPNMMD---EDTHAHLTPEAPELLERYK
R.p. NuoE IK--HKETTKDQKFTLSEIECLGAVN-APVVQIN---DDYEDLNEMAKMEKLEIQYLNKFKSK
N.c. 24 kDa IK--QGETTPDGLFTFIEVECLGAVN-APMVQIN---DDYEDLTPETIKQVLSALKESVTDVSKAPQPGPQS (28)
H.s. 24 kDa IK--VGETTPDKLFTLIEVECLGAVN-APMVQIN---DNYEDLTKADIEEII DELKAGKIPKPGPRSGRFSC (24)
N.o. 24 kDa IK--MGGTTKDGMFTLEVECLGAVN-APMVQIN---NEKYVEDLTPETIMPEMLEKFRKGEIKAGPQTKGRK (45)
N.o. PA HDG VNDLHSSVSRDGFTHFTMNWLGVCVNDGPAMMKRRGGDYVEVLTLGLTGDGVEQS---LKLKGNVFWKAKNK
N.o. BD HDG VQDFHGSVSKNGKFTFHGMNWLGYCVNDGPAMLIKRTGGDYVETLTLGLSGDNIIES---LNSLKGKTYKWKANN
N.o. PB HDG VQDFHGSVSKNGKFTFHGMNWLGYCVNDGPAMLIKRTGGDYVETLTLGLSGDNIIES---LNSLKGKTYKWKANN
N.o. BA HDG INKTHGGVAKDGSFTLHNLWLGVCVNDGPAMMIKRTGTYVETFTGLLEDNIDQRRLKLDKDLKELPKWPKNN
N.o. PD HDG INKTHGGVAKDGSFTLHNLWLGVCVNDGPAMMIKRTGTYVETFTGLLEDNIDQRRLKLDKDLKELPKWPKNN
N.o. PN HDG IHETHGGVAKDGSFTLHNLWLGVCVNDGPAMMIKRTGTYVETFTGLLEDNIDQRRLKLDKDLKELPKWPKNN
R.o. HoxF AR--FGGTDKTGMFGLFETPCIGLSDQ-EPAMLIDNVVFTRLRPGTIVDIITQLRQGRSPEDIANPAGLPSDDV (436)
R.e. HoxF IR--FGETDPNGMFLDFTPCIGLSDQ-EPAMLIDKVVFTRLRPGKIVDIIAQLKQGRSPAEIANPAGLPSQDI (434)

B

NADH binding domain

-----G-GG-G-----
E. coli NuoF (22) PVWLDEYRSKNGYEGA-----RKALTLGLSPDEIVNQVKDAGLKRGGAGFSTGLKWSLMPKDESMNIRYLL
R. prowazekii NuoF (17) YDLKSSQKRGDWYN-----TKALIDKGRDFIDEVKKSLGRGGAGFSTGLKWSLMPKNS-EKFCYLV
H. sapiens 51 kDa (50) WRLKGSLSRGGDWYK-----TKELILKGPDWLGEIKTSLGRGGAGFSTGLKWSLMPKNSRGRFPLYV
Euplotes sp. 51 kDa (47) PFIDGALKRGRDWHK-----TKDIVLNGDDWIDQIKASGLRGRGGAGFSTGLKWSLMPKNSRGRFPLYV
N. ovalis PA 51 kDa (50) PFIDGALKRGRDWHK-----TKDIVLNGDDWIDQIKASGLRGRGGAGFSTGLKWSLMPKNSRGRFPLYV
N. ovalis BA 51 kDa (49) PFINGALKRGRDWHK-----TKDIVLNGDDWIDQIKASGLRGRGGAGFSTGLKWSLMPKNSRGRFPLYV
N. ovalis BD HDG IVEQSLKSKGKEYSLENIHISVKDAIKKAVQMGSMKVIKEVTEAKLLGRGGAGFMTGRKWESEYKADV-KEYYV
N. ovalis PB HDG IVEQSLKSKGKEYSLENIHISVKDAIKKAVQMGSMKVIKEVTEAKLLGRGGAGFMTGRKWESEYKADV-KEYYV
N. ovalis BA HDG IKEMRSQRDNGYSCMNTQAPIAEATKKAVSMGPEKVEIEIFKSNLVGRGGAGFRTGKWESEYKTPA-TDKYVV
N. ovalis PD HDG IKEMRSQRDNGYSCMNTQAPIAEATKKAVSMGPEKVEIEIFKSNLVGRGGAGFRTGKWESEYKTPA-TDKYVV
N. ovalis PN HDG IKEMRSQRDNGYSCMNTQAPIAEATKKAVSMGPEKVEIEIFKSNLVGRGGAGFRTGKWESEYKTPA-TDKYVV
R. opacus HoxU (173) VVESNVRTKGPVFRGLTDYG--RLELCLALRPEQIIDRIIESKLRGRGGAGFSTGLKWLQCRTAVS-DDKYII
R. eutropha HoxU (173) MVESNVRTKGPVFRGRDTRLR--SLDDQCLLLKPEQIETIVDSRLRGRGGAGFSTGLKWLRCRAES-EQKYVI

E.c. NuoF CNADEMEPGTYKDRLLMEQLP--HLLVEGLMISAFALKAYRGIYFLRGEYIEAAVNLRRATAEATEAGLLGKNI-MGTGFDFE
R.p. NuoF VNADESEPGTCKDRILRHP--HKLIEGLCLIASFAIGANTCYIYIRGEFYNEASNMQRALDEAYKEGLIGKNA-CGSGYDFD
H.s. 51 kDa VNADEGEPTCKDREILRHP--HKLIEGLCLVGGGRAMGARAAYIYIRGEFYNEASNLQVAIREAYEAGLIGKNA-CGSGYDFD
E.sp. 51 kDa INADESEPGTCKDREIMRHP--HKLIEGALqVqVSMRAKAAAYIYIRGEFYQVNCLERAISEAYERGLIGKNA-CGTGYDFD
N.o. PA 51 kDa VNADESEPATCKDREIMRHP--HKLIEGALIVGYAMRAKAAAYVYIRGEFWEAQQLERAVAEAYEKGFIGKNA-CGSGYDFD
N.o. BA 51 kDa VNADESEPATCKDREIMRHP--HKLIEGALIVGYAMRAKAAAYVYIRGEFWEAQQLERAVAEAYEKGFIGKNA-CGSGYDFD
N.o. BD HDG CNADEGLPSTFKDWYLLNENKREKVLGAGMIGCANTIGAKKCYLYLRYEYRNLVPIEADIKKLQSE-----CPELAMLN
N.o. PB HDG CNADEGLPSTFKDWYLLNENKREKVLGAGMIGCANTIGAKKCYLYLRYEYRNLVPIEADIKKLQSE-----CPELAMLN
N.o. BA HDG CNADEGLPSTYKDWCLLNHEVKKRKEVFTGMGICAKTIGAKRCFLYLYRYEYRNLVPALEQAIKDVQRT-----CPELADLK
N.o. PD HDG CNADEGLPSTYKDWCLLNHEVKKRKEVFTGMGICAKTIGAKRCFLYLYRYEYRNLVPALEQAIMDVQRT-----CPELADLK
N.o. PN HDG CNADEGLPSTYKDWCLLNHEVKKRKEVFTGMGICAKTIGAKRCFLYLYRYEYRNLVPALEQSIKDVQRT-----CPELADLK
R.o. HoxU CNADEGEPTFKDRVLLTRSP--KKVFMGMIAARAIGSRNGLLYLRWEYIYLDKYLRLQELRDEGLLGRIGGSGDFD
R.e. HoxU CNADEGEPTFKDRVLLTRAP--KKVFMGMIAARAIGCRKIVYLYRGEYFYLKDYLRQLQELRDEGLLGRIGGSGDFD

FMN binding site

G-G---G-----G---P---PP---P-----P-----
 E.c. NuoF LFVHTGAGRYICGEETALINSLEGRANRERKPE---FFATSGVWGKPTCVNNVETLCNVPAILANGVEWYQNIKSKSDAGTK
 R.p. NuoF IYLRHAGAYICGEETALLESLEKKGKMRKLPKPE---FFAGFGLYGCPTTINNVEISIAVVPITILRRGASWFAAIGKPNNTGTK
 H.s. 51 kDa VVVRHAGAYICGEETALIESIEGKQKGRKLPKPE---FFADVGVGCPPTVANVETVAVSPTICRRGGTWFAGFGRERNSTGK
 E.sp. 51 kDa VHVHAGAYICGEETGLIESLEGGKQKGRKLPKPE---FFANAGLYGCPTTNNVETVAVCPITILRRTPWVAFSFGGRKNNAGTK
 N.o. PA 51 kDa IYVHRGAGAYICGEETSMLSSIEGVIGKPRMKPE---YFAGTGLYGCPTTNNVETVSTVPTIMRRGGWFASFGRKNNHGTK
 N.o. BA 51 kDa IYVHRGAGAYICGEETSMLSSIEGVIGKPRMKPE---YFAGTGLYGCPTTNNVETVSTVPTIMRRGGWFASFGRKNNHGTK
 N.o. BD HDG YEVRLLGGGPPYVAGEENAQFESIQGSAPIRKRDRSSVFFTEIEGLFFKPTVINNVETFAACVPHIVQOGSAAFKTNGLP-----K
 N.o. PB HDG YEVRLLGGGPPYVAGEENAQFESIEGRAPLRKRDRFGNVFFTEIEGLFFKPTVINNVETFAACVPHIVQOGSAAFKTNGLP-----K
 N.o. BA HDG YEIRLLGGGPPYVAGEENAQFESIEGRAPLRKRDRFGNVFFTEIEGLFFKPTVINNVETFAAVPHIIQOGSQDFEGEGKMP-----K
 N.o. PD HDG YEIRLLGGGPPYVAGEENAQFESIEGRAPLRKRDRFGNVFFTEIEGLFFKPTVINNVETFAAVPHIIQOGSQDFEGEGKMP-----K
 N.o. PN HDG YEIRLLGGGPPYVAGEENAQFESIEGRAPLRKRDRFGNVFFTEIEGLFFKPTVINNVETFAAVPHIIQOGSQDFEGEGKMP-----K
 R.o. HoxU IRIQMAGAGAYICGDESALIESCEGKRGTFRVKPE---FFVQEGYLKPTCVNNVETFAAAARIMEEGPNWFRALGTPSTGTR
 R.e. HoxU IRIQMAGAGAYICGDESALIESCEGKRGTFRVKPE---FFVQEGYLKPTCVNNVETFAAVSRIMEEGADWFRAMGTPDSAGTR

E.c. NuoF LMGFSGRVKNPLWELPFGTTAREILEDYAGGMRDGLK-FKAWQPGGAGTDFLTEAHL-DLPMEFESIGKAGSRLGTALAMAV
 R.p. NuoF VFCISGHVNMPCNIEEVMCVLKELEKXVAGGVGGWNNLKAIPGGASVPLLPKSLCE-VEMDFDLSLRTVGSGLCTGGIIVM
 H.s. 51 kDa LFNISGHVNHPCVTEEEMSVLKELEKXVAGGVGGWNNLKAIPGGASVPLLPKRIICDDVLMDFDALRDVRSGLGTAIVM
 E.sp. 51 kDa LFAVSGHVNNPVGFEEMSIPLRELIEKHGGVGGWNNLKAIPGGASVPLLPKRIICDDVLMDFDALRDVRSGLGTAIVM
 N.o. PA 51 kDa LYCLSGHINNPCTVEDEMSISLRELIERHGGVGGWNNLKAIPGGASVPLLPKRIICDDVLMDFDALRDVRSGLGTAIVM
 N.o. BA 51 kDa LYSLSGHINNPCTVEDEMSISVRELIERHGGVGGWNNLKAIPGGASVPLLPKRIICDDVLMDFDALRDVRSGLGTAIVM
 N.o. BD HDG LLSVSGDVERPLIIECLLNG---YTLNLDLIDAKARD-VAAAEIGGCTEPLVFDKFS--MP-FGFGKVLNAA--SVVLF
 N.o. PB HDG LLSVSGDVERPLIIECLLNG---YTLNLDLIDAKARD-VAAAEIGGCTEPLVFDKFS--MP-FGFGKVLNAA--SVVLF
 N.o. BA HDG LLSVTDGVEQPILIEHLN---YSLNHLLEIDAKD-IVAAEIGGCTEPIIFGSKFD--TL-FGFGKGLNAAV--SVVLF
 N.o. PD HDG LLSVTDGVDAPILFETHLNN---YSLNHLLEIDAKD-IVAAEIGGCTEPIIFGSKFD--TL-FGFGKGLNAAV--SVVLF
 N.o. PN HDG LLSVTDGVDPEPILIEHLN---YSLNHLLEISAKD-IVAAEIGGCTEPIIFGSKFD--TL-FGFGKGLNAAV--SVVLF
 R.o. HoxU LLSVAGDCSRPGIYEVEWGV---TLNEVLTIVGARD-ARAVQISGSPGQCVSVAEDG--ER--RMAYEDISGNG--AFTIF
 R.e. HoxU LLSVAGDCSKPGIYEVEWGV---TLNEVLTIVGARD-ARAVQISGSPGQCVSVAEDG--ER--KLAYEDLSGNG--AFTIF

[4Fe-4S]cluster N3 of 51 kDa and NuoF

C-C-C-----C-----C-----
 E.c. NuoF DHEINMVSILVRNLEEFFFARESGCGCTPCRDGLPWSVKILRALEREGQPGDIETLEQLCRFLGPKTFCAHAPGAVEPLQSAI
 R.p. NuoF DKSTDIYAIARLSKFKYMHESCGGCTPCREGTGWMMWRVMMRLVNGNAKNEIDTLNVTKEI-EGHTICALGDAAAWPVQGLI
 H.s. 51 kDa DRSTDIVKAIARLIEFKHESCGGCTPCREGVDMNKMVMARFVRGDARPAEIDSLWEISKQI-EGHTICALGDAAAWPVQGLI
 E.sp. 51 kDa DKSTDVIAAIHRLSKFYAHESCGGCTPCREGTSWMDMLGRMRKGNADFAEIDMLEELSYQI-EGHTICALGDAAAWPVQGLI
 N.o. PA 51 kDa DKSTDVIDAILRLSKFYLHESCGGCTPCREGTGWLVDLIERMKIGKADYGEIDQLYELTKQI-EGHTICALGEAAAWPVQGLI
 N.o. BA 51 kDa DKSTDVIDAILRLSKFYLHESCGGCTPCREGTGWLVDLIERMKIGKADYGEIDQLYELTKQI-EGHTICALGEAAAWPVQGLI
 N.o. BD HDG DTACDFGEVYSNKLHFMADSECKQCVPCRDGAQLLHKAFDQMRRTGKTKYNERSLKTAEEA-KLSAICAHGKALNPLDSDAC
 N.o. PB HDG DTACDFGEVYSNKLHFMADSECKQCVPCRDGAQLLHKAFDQMRRTGKTKYNERSLKTAEEA-KLSAICAHGKALNPLDSDAC
 N.o. BA HDG NSSCDLGIYENKLFMSEESCKQCVPCRDGSYIFHRAFKELRDGTGKSSYNMRALSVASEA-ARSSICAHGKALEGLVKAAP
 N.o. PD HDG NSSCDLGIYENKLFMSEESCKQCVPCRDGSYIFHRAFKELRDGTGKSSYNMRALSVASEA-ARSSICAHGKALEGLVKAAP
 N.o. PN HDG NSSCDLGIYENKLFMAEESCKQCVPCRDGSYIFHRAFKELRDGTGKSSYNMRALSVASEA-ARSSICAHGKALESLFKSAC
 R.o. HoxU NTERDLLEIVKDFMQFFVDESCKQCVPCRVGNIDLHKKVELVIAGKACQKDLDDVVSAGALV-KKTSRGLGATSPNPIILTTL
 R.e. HoxU NCKRDLEIVRDMQFFVEESCKQCVPCRVGNVDLHRKVEVVIAGKACQKDLDDVVSAGALV-RRTSRGLGATSPKPIILTTL

E.c. NuoF KYFREFEAGIKQPFNSNTHLINGIQPNLLKERW
 R.p. NuoF RHRFDEIEQRKISFGIA
 H.s. 51 kDa RHRFPELEERMQRFAQQHQARQAAS
 E.sp. 51 kDa RHRFHMEDRIEDYKAENFERGQRAKVSHLPEHH
 N.o. PA 51 kDa KHYRDVIEDRIDKYHSEHPAAAEFII SHHPVKGTH
 N.o. BA 51 kDa KHYRPMEDRMDKYHSQHPVVAEGPFSHHHPVAGSH
 N.o. BD HDG EYLSKSKPL
 N.o. PB HDG EYLSKSKPL
 N.o. BA HDG DFMNKTTPNY
 N.o. PD HDG DFMNKTTPSY
 N.o. PN HDG DFMNKTTPYI
 R.o. HoxU DKFPEIYTKRLRQKKEALLSFDLDAALGGYEKALEGLAKEEIK
 R.e. HoxU EKFPFIYQNKLVREHGP-LLPSFDLDAALGGYEKALKDLEEVTR